

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 01/557-745

Source: US

Date Processed by STIC: 11/19/98

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

**<http://www.uspto.gov/web/offices/pac/checker>**

PCT09

## RAW SEQUENCE LISTING

DATE: 10/30/2001

PATENT APPLICATION: US/09/856,543

TIME: 13:16:02

Input Set : A:\01632002.app

Output Set: N:\CRF3\10302001\I856543.raw

JES 000 Copy

Corrected Diskette Needed

3 <110> APPLICANT: Hartwich, Gerhard  
 4 Heller, Adam  
 6 <120> TITLE OF INVENTION: METHOD FOR THE ELECTROCHEMICAL DETECTION OF NUCLEIC  
 7 ACID OLIGOMER HYBRIDS  
 9 <130> FILE REFERENCE: 0163-2002  
 11 <140> CURRENT APPLICATION NUMBER: 09/856,543  
 12 <141> CURRENT FILING DATE: 1999-11-19  
 14 <150> PRIOR APPLICATION NUMBER: PCT/EP99/08888  
 15 <151> PRIOR FILING DATE: 1998-11-23  
 17 <160> NUMBER OF SEQ ID NOS: 2  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 12  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Unknown  
 26 <220> FEATURE:  
 W--> 28 <223> OTHER INFORMATION: *→ multiple explanations, see error Summary sheet, Item 11*  
 28 <400> SEQUENCE: 1  
 29 Thr Ala Gly Thr Cys Gly Gly Ala Ala Gly Cys Ala  
 30 1 5 10  
 33 <210> SEQ ID NO: 2  
 34 <211> LENGTH: 12  
 35 <212> TYPE: PRT  
 36 <213> ORGANISM: Unknown  
 38 <220> FEATURE:  
 W--> 40 <223> OTHER INFORMATION: *assume*  
 40 <400> SEQUENCE: 2  
 41 Ala Thr Cys Ala Gly Ala Thr Thr Thr Cys Gly Thr  
 42 1 5 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/856,543

DATE: 10/30/2001

TIME: 13:16:03

Input Set : A:\01632002.app

Output Set: N:\CRF3\10302001\I856543.raw

L:28 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

L:40 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

## Raw Sequence Listing Error Summary

### ERROR DETECTED     SUGGESTED CORRECTION

SERIAL NUMBER: 091886543

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping".  
     Wrapped Aminos
- 2 ☐ Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.  
     Numbering
- 4 ☐ Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**  
     "bug"
- 7 ☐ Skipped Sequences     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence.  
     (OLD RULES)     (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                           (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                           This sequence is intentionally skipped  
  
                           Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences     Sequence(s)        missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
     (NEW RULES)     <210> sequence id number  
                           <400> sequence id number  
                           000
- 9 ☐ Use of n's or Xaa's     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)     Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                           In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents
- 10 ☐ Invalid <213>     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or  
     Response     scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220>     Sequence(s) 1+2 missing the <220> "Feature" and associated numeric identifiers and responses.  
                           Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                           (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk  
     "bug"